

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

Best Available Copy

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/687,204B
Source: FWO
Date Processed by STIC: 3/3/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05





Raw Sequence Listing Error Summary

SERIAL NUMBER: 10/687,204B

ERROR DETECTED

SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 16, 10, 11, 13 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/687,204B

DATE: 03/03/2005

TIME: 11:02:42

Input Set : A:\13-118 Seq list Final.txt

Output Set : N:\CRF4\03032005\J687204B.raw

3 <110> APPLICANT: Boehringer Ingelheim International GmbH
 5 <120> TITLE OF INVENTION: Composition for the Treatment of
 6 Infection by Flaviviridae Viruses
 9 <130> FILE REFERENCE: 13/118
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/687,204B
 C--> 12 <141> CURRENT FILING DATE: 2003-10-16
 14 <150> PRIOR APPLICATION NUMBER: US 60/421,900
 15 <151> PRIOR FILING DATE: 2002-10-29
 17 <160> NUMBER OF SEQ ID NOS: 16
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

208 <210> SEQ ID NO: 16
 209 <211> LENGTH: 9
 210 <212> TYPE: PRT
 211 <213> ORGANISM: Artificial Sequence
 213 <220> FEATURE:
 214 <221> NAME/KEY: VARIANT
 215 <222> LOCATION: 1, 3, 6, 9
 217 <223> OTHER INFORMATION: Xaa at position 1 is acetylated-Asp
 219 <223> OTHER INFORMATION: Xaa at position 3 is Asp (EDANS)
 221 <223> OTHER INFORMATION: Xaa at position 6 is amino butyric acid [C(O)-O]
 223 <223> OTHER INFORMATION: Xaa at position 9 is Lys[DABCYL]
 W--> 225 <400> 16
 W--> 226 Xaa Glu Xaa Glu Glu Xaa Ala Ser Xaa
 227 1 5
 E--> 232 4 delete

pp 1-2
 Does Not Comply
 Corrected Diskette Needed.

needs explanation in 22207-22237 section
 (see item 11 on Error Summary
 sheet)

same
 error
 in sequence 10,
 sequence 11,
 sequence 13

14/08/2015 2



<110> Boehringer Ingelheim International GmbH

<120> Composition for the Treatment of
Infection by Flaviviridae Viruses

range
to
<130> 13/118
<150> ~~<150>~~ US 60/442,769
<151> ~~<151>~~ 2003-01-27

<140> US 10/687,204
<141> 2003-10-16

here
we
prior data
<150> US 60/421,900
<151> 2002-10-29

VERIFICATION SUMMARY

DATE: 03/03/2005

PATENT APPLICATION: US/10/687,204B

TIME: 11:02:43

Input Set : A:\13-118 Seq list Final.txt

Output Set: N:\CRF4\03032005\J687204B.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:58 M:283 W: Missing Blank Line separator, <220> field identifier
L:133 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:225 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:232 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16